

#4



PCT

## RAW SEQUENCE LISTING

DATE: 08/26/2004

PATENT APPLICATION: US/10/505,315

TIME: 16:07:19

Input Set : A:\60163PCT SEQ listing.txt

Output Set: N:\CRF4\08262004\J505315.raw

3 <110> APPLICANT: Syngenta Participations AG  
4 Shen, Zhicheng  
5 Warren, Gregory  
6 Shotkoski, Frank  
7 Kramer, Vance  
9 <120> TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use  
11 <130> FILE REFERENCE: 60163PCT  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/505,315  
C--> 13 <141> CURRENT FILING DATE: 2004-08-19  
13 <150> PRIOR APPLICATION NUMBER: US 60/362250  
14 <151> PRIOR FILING DATE: 2002-03-06  
16 <160> NUMBER OF SEQ ID NOS: 33  
18 <170> SOFTWARE: PatentIn version 3.2  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 2367  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Bacillus thuringiensis  
26 <220> FEATURE:  
27 <221> NAME/KEY: misc\_feature  
28 <222> LOCATION: (1)..(2367)  
29 <223> OTHER INFORMATION: Native vip3C coding sequence.  
30 An "r" at position 2213 represents the nucleotide g or a.  
32 <400> SEQUENCE: 1  
33 atgaacaaga ataatactaa attaagcaca agagccctac cgagttttat tgattatttt 60  
35 aatggcattt atggatttgc cactgggtatc aaagacatta tgaatatgat ttttaaaacg 120  
37 gatacagggtg gtaatctaac cttagacgaa atcctaaaga atcagcagtt actaaatgag 180  
39 atttctggta aattggatgg ggtaaattggg agcttaaattg atcttatcgc acaggggaaac 240  
41 ttaaatacag aattatctaa ggaaatctta aaaatcgcaa atgaacagaa tcaagtctta 300  
43 aatgatgtta ataacaaact cgatgcgata aatacgatgc ttcatatata tctacctaaa 360  
45 attacatcta tgtaagtga tgtaatgaag caaaattatg cgctaagtct gcaaatagaa 420  
47 tacttaagta agcaattgca agaaatttct gataaattag atattattaa cgtaaattgt 480  
49 cttattaact ctacacttac tgaaattaca cctgcataac aacggattaa atatgtgaat 540  
51 gaaaaatttg aagaattaac ttttgctaca gaaaccactt taaaagtaaa aaaggatagc 600  
53 tcgcctgctg atattcttga tgagttaact gaattaactg aactagcgaa aagtgttaca 660  
55 aaaaatgacg ttgatgggtt tgaattttac cttaatatcat tccacgatgt aatggtagga 720  
57 aataatttat tcgggcgttc agctttaaaa actgcttcag aattaattgc taaagaaaat 780  
59 gtgaaaacaa gtggcagtga agtaggaaat gtttataatt tcttaattgt attaacagct 840  
61 ctacaagcaa aagcttttct tactttaaca acatgccgaa aattattagg cttagcaggt 900  
63 attgattata cttctattat gaatgaacat ttaaataagg aaaaagagga atttagagta 960  
65 aacatccttc ctacactttc taatactttt tctaactcta attatgcaaa agttaaagga 1020  
67 agtgatgaag atgcaaagat gattgtggaa gctaaaccag gacatgcatt ggttggtttt 1080  
69 gaaatgagca atgattcaat cacagtatta aaagtatatg aggctaagct aaaacaaaat 1140  
71 tatcaagttg ataaggattc cctatcggag gttattttat gtgatacggg taaattattt 1200



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73 tgtccagatc aatctgaaca aatatattat acaaataaca tagtattccc aaatgaatat 1260
75 gtaattacta aaattgattt cactaaaaaa atgaaaactt taagatatga ggtaacagcg 1320
77 aatttttatg attcttctac aggagaaatt gacttaaata agaaaaaagt agaatcaagt 1380
79 gaagcggagt atagaacgtt aagtgtctat gatgatggag tgtatatgcc attaggtgtc 1440
81 atcagtgaaa cttttttgac tccgataaat gggtttggcc tccaagctga tgaaaattca 1500
83 agattaatta cttaacatg taaatcatat ttaagagaac tactgtctagc aacagactta 1560
85 agcaataaag aaactaaatt gatcgctcca ccaagtgggt ttattagcaa tattgtagag 1620
87 aacgggtcca tagaagagga caatttagag ccgtggaaag caaataataa gaatgcgtat 1680
89 gtagatcata caggcggagt gaatggaact aaagctttat atgttcataa ggacggagga 1740
91 ttttcacaat ttattggaga taagttaaaa ccgaaaactg agtatgtaat ccaatatact 1800
93 gttaaaggaa aaccttctat tcatttaaaa gatgaaaata ctggatatat tcattatgaa 1860
95 gatacaaata ataatttaaa agattatcaa actattacta aacgttttac tacaggaact 1920
97 gatttaaaagg gagtgtattt aatttttaaa agtcaaaatg gagatgaagc ttggggagat 1980
99 aaatttacaa ttttagaaat taagcctgcg gaggatttat taagcccaga attaattaat 2040
101 ccgaattctt ggattacgac tccaggggct agcatttcag gaaataaact tttcattaac 2100
103 ttggggacaa atgggacctt tagacaaagt ctttcattaa acagttattc aacttatagt 2160
105 ataagcttta ctgcatcagg accatttaat gtgacggtaa gaaattctag ggragtatta 2220
107 tttgaacgaa gcaaccttat gtcttcaact agtcatattt ctgggacatt caaaactgaa 2280
109 tccaataata ccgattata tgtagaactt tcccgtcgct ctggtggtgg tggatcata 2340
111 tcatttgaaa acgtttctat taaataa 2367
114 <210> SEQ ID NO: 2
115 <211> LENGTH: 788
116 <212> TYPE: PRT
117 <213> ORGANISM: Bacillus thuringiensis
120 <220> FEATURE:
121 <221> NAME/KEY: MISC_FEATURE
122 <222> LOCATION: (1)..(788)
123 <223> OTHER INFORMATION: Vip3C Toxin
124 The Xaa at position 738 is either the amino acid Glu or Gly.
126 <400> SEQUENCE: 2
128 Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro Ser Phe
129 1 5 10 15
132 Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp
133 20 25 30
136 Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asn Leu Thr Leu
137 35 40 45
140 Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Glu Ile Ser Gly Lys
141 50 55 60
144 Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
145 65 70 75 80
148 Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln
149 85 90 95
152 Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr
153 100 105 110
156 Met Leu His Ile Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val
157 115 120 125
160 Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys
161 130 135 140
164 Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val

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165 145          150          155          160
168 Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile
169          165          170          175
172 Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr
173          180          185          190
176 Thr Leu Lys Val Lys Lys Asp Ser Ser Pro Ala Asp Ile Leu Asp Glu
177          195          200          205
180 Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val
181          210          215          220
184 Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly
185 225          230          235          240
188 Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile
189          245          250          255
192 Ala Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
193          260          265          270
196 Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr
197          275          280          285
200 Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Gly Ile Asp Tyr Thr
201          290          295          300
204 Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val
205 305          310          315          320
208 Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala
209          325          330          335
212 Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys
213          340          345          350
216 Pro Gly His Ala Leu Val Gly Phe Glu Met Ser Asn Asp Ser Ile Thr
217          355          360          365
220 Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp
221          370          375          380
224 Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Thr Asp Lys Leu Phe
225 385          390          395          400
228 Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe
229          405          410          415
232 Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
233          420          425          430
236 Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
237          435          440          445
240 Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr
241          450          455          460
244 Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val
245 465          470          475          480
248 Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala
249          485          490          495
252 Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
253          500          505          510
256 Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile
257          515          520          525
260 Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile
261          530          535          540

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264 Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr
265 545 550 555 560
268 Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
269 565 570 575
272 Lys Asp Gly Gly Phe Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys
273 580 585 590
276 Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His
277 595 600 605
280 Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn
281 610 615 620
284 Asn Leu Lys Asp Tyr Gln Thr Ile Thr Lys Arg Phe Thr Thr Gly Thr
285 625 630 635 640
288 Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu
289 645 650 655
292 Ala Trp Gly Asp Lys Phe Thr Ile Leu Glu Ile Lys Pro Ala Glu Asp
293 660 665 670
296 Leu Leu Ser Pro Glu Leu Ile Asn Pro Asn Ser Trp Ile Thr Thr Pro
297 675 680 685
300 Gly Ala Ser Ile Ser Gly Asn Lys Leu Phe Ile Asn Leu Gly Thr Asn
301 690 695 700
304 Gly Thr Phe Arg Gln Ser Leu Ser Leu Asn Ser Tyr Ser Thr Tyr Ser
305 705 710 715 720
308 Ile Ser Phe Thr Ala Ser Gly Pro Phe Asn Val Thr Val Arg Asn Ser
309 725 730 735
W--> 312 Arg Xaa Val Leu Phe Glu Arg Ser Asn Leu Met Ser Ser Thr Ser His
313 740 745 750
316 Ile Ser Gly Thr Phe Lys Thr Glu Ser Asn Asn Thr Gly Leu Tyr Val
317 755 760 765
320 Glu Leu Ser Arg Arg Ser Gly Gly Gly His Ile Ser Phe Glu Asn
321 770 775 780
324 Val Ser Ile Lys
325 785
328 <210> SEQ ID NO: 3
329 <211> LENGTH: 2367
330 <212> TYPE: DNA
331 <213> ORGANISM: Artificial Sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Maize optimized vip3C coding sequence.
335 An "r" at positions 2213 and 2214 represents the nucleotide g or
336 a.
338 <400> SEQUENCE: 3
339 atgaacaaga acaacaccaa gctctccacc cgcgcctcc cgctcttcat cgactacttc 60
341 aacggcatct acggcttcgc caccggcatc aaggacatca tgaacatgat cttcaagacc 120
343 gacaccggcg gcaacctcac cctcgacgag atcctcaaga accagcagct cctcaacgag 180
345 atcagcggca agctcgacgg cgtgaacggc tccctcaacg acctcatcgc ccagggcaac 240
347 ctcaacaccg agctgtccaa ggagatcctc aagatcgcca acgagcagaa ccaggtgctc 300
349 aacgacgtga acaacaagct cgacgccatc aacaccatgc tccacatcta cctcccgaag 360
351 atcacctcca tgctctccga cgtgatgaag cagaactacg ccctctccct ccagatcgag 420
353 tacctctcca agcagctcca ggagatcagc gacaagctcg acatcatcaa cgtgaacgtg 480

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355 ctcatcaact ccaccctcac cgagatcacc cggcctacc agcgcacaa gtacgtgaac 540
357 gagaagttcg aggagctgac cttcgccacc gagaccaccc tcaaggtgaa gaaggactcc 600
359 tccccggccg acatcctcga cgagctgacc gagctgaccg agctggccaa gtccgtgacc 660
361 aagaacgacg tggacggctt cgagttctac ctcaacacct tccacgacgt gatggtgggc 720
363 aacaacctct tcggccgctc cgccctcaag accgcctccg agctgatcgc caaggagaac 780
365 gtgaagacct cgggctccga ggtgggcaac gtgtacaact tctcatcgt gtcaccgcc 840
367 ctgcaggcca aggccttctt caccctcacc acctgccgca agctcctcgg cctcgccggc 900
369 atcgactaca cctccatcat gaacgagcac ctcaacaagg agaaggagga gttccgcgtg 960
371 aacatcctcc cgaccctctc caacaccttc tccaaccgga actacgcaa ggtgaagggc 1020
373 tccgacgagg acgccaagat gatcgtggag gccaaagccg gccacgccct cgtgggcttc 1080
375 gagatgtcca acgactccat caccgtgctc aagggtgtac aggccaaagt caagcagaac 1140
377 taccaggtgg acaaggactc cctctccgag gtgatctacg gcgacaccga caagctcttc 1200
379 tgcccgacc agtccgagca gatatactac accaacaaca tcgtgttccc gaacgagtac 1260
381 gtgatcacca agatcgactt caccaagaag atgaagaccc tccgctacga ggtgaccgcc 1320
383 aacttctacg actcctccac cggcgagatc gacctcaaca agaagaagg ggagtccctc 1380
385 gaggcgagat accgcacct ctccgccaac gacgacggcg tgtacatgcc gctcggcgtg 1440
387 atctccgaaa ccttcctcac cccgatcaac ggcttcggcc tccaggccga cgagaactcc 1500
389 cgctcatca ccctcacctg caagtcctac ctccgcgagc tgctcctcgc caccgacctc 1560
391 tccaacaagg agaccaagct catcgtgccg ccgtccggct tcatctccaa catcgtggag 1620
393 aacggctcca tcgaggagga caacctcgag ccgtggaagg ccaacaacaa gaacgcctac 1680
395 gtggaccaca cgggcggcgt gaacggcacc aaggccctct acgtgcacaa ggacggcggc 1740
397 ttctcccagt tcatcggcga caagctcaag ccgaagaccg agtacgtgat ccagtacacc 1800
399 gtgaagggca agcgtccat ccacctcaag gacgagaaca ccggctacat ccactacgag 1860
401 gacaccaaca acaacctcaa ggactaccag accatcacca agcgttcac caccggcacc 1920
403 gacctcaagg gcgtgtacct catcctcaag tcccagaacg gcgacgaggc ctggggcgac 1980
405 aagttcacca tccttgagat caagccggcc gaggacctcc tctcccggga gctgatcaac 2040
407 ccgaactcct ggatcaccac cccgggcgcc tccatctccg gcaacaagct cttcatcaac 2100
409 ctccgcacca acggcacctt ccgccagtc ctctcctca actcctactc cacctactcc 2160
411 atctccttca ccgcctccgg ccggttcaac gtgaccgtgc gcaactcccg cgrtgtgctc 2220
413 ttcgagcgct ccaacctcat gtctccacc tcccacatct ccggcacctt caagaccgag 2280
415 tccaacaaca ccggcctcta cgtggagctg tcccgcgct ccggcgggcg cggccacatc 2340
417 tccttcgaga acgtgtccat caagtag 2367
420 <210> SEQ ID NO: 4
421 <211> LENGTH: 2370
422 <212> TYPE: DNA
423 <213> ORGANISM: Bacillus thuringiensis
426 <220> FEATURE:
427 <221> NAME/KEY: misc_feature
428 <222> LOCATION: (1)..(2370)
429 <223> OTHER INFORMATION: vip3A(a) native coding sequence.
431 <400> SEQUENCE: 4
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436 gatacaggtg gtgatctaac cctagacgaa attttaaaga atcagcagtt actaaatgat 180
438 atttctggta aattggatgg ggtgaatgga agcttaaagt atcttatcgc acagggaaac 240
440 ttaaatacag aattatctaa ggaaatatta aaaattgcaa atgaacaaaa tcaagtttta 300
442 aatgatgtta ataacaaact cgatgcgata aatacgatgc ttcgggtata tctacctaaa 360
444 attacctcta tgttgagtga tgtaatgaaa caaaattatg cgctaagtct gcaaatagaa 420
446 tacttaagta aacaattgca agagatttct gataagttgg atattattaa tgtaaatgta 480

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/505,315

DATE: 08/26/2004  
TIME: 16:07:20

Input Set : A:\60163PCT SEQ listing.txt  
Output Set: N:\CRF4\08262004\J505315.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 738

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/505,315

DATE: 08/26/2004

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Input Set : A:\60163PCT SEQ listing.txt

Output Set: N:\CRF4\08262004\J505315.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:736